

0360
20/0590

#2



RAW SEQUENCE LISTING

DATE: 03/05/2002

PATENT APPLICATION: US/09/784,810A

TIME: 09:56:39

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 6 SAME
 8 <130> FILE REFERENCE: 10716-08
 10 <140> CURRENT APPLICATION NUMBER: 09/784,810A
 11 <141> CURRENT FILING DATE: 2001-02-14
 13 <150> PRIOR APPLICATION NUMBER: 60/182,360
 14 <151> PRIOR FILING DATE: 2000-02-14
 16 <150> PRIOR APPLICATION NUMBER: 60/191,261
 17 <151> PRIOR FILING DATE: 2000-03-22
 19 <160> NUMBER OF SEQ ID NOS: 29
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 29 <221> NAME/KEY: modified_base
 30 <222> LOCATION: (1)
 31 <223> OTHER INFORMATION: a, t, c, g, other or unknown
 33 <400> SEQUENCE: 1

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 36 cagcgcccc acagcgccag ggacccctg gcagcgggag ccgcggtcg aggttatgga 180
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58 aaggggtgaga aggtggaggc tatgctttgg ggggacaggc cagaatgaag tcctgggtca 1500
59 ggagcccagc tggctgggcc cagctgccta tgtaaggcct tctagtttgt tctgagaccc 1560
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73 20 25 30
75 Leu Phe Arg Ser His Val Gln Pro Leu Leu Ala Glu Ala Glu Ile Ser
76 35 40 45
78 Phe Thr Leu Met Leu Thr Glu Arg Arg Asn His Ala Arg Glu Leu Val
79 50 55 60
81 Arg Ser Glu Glu Leu Gly Arg Trp Asp Ala Leu Val Val Met Ser Gly
82 65 70 75 80
84 Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
85 85 90 95
87 Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Ala Gly Ser
88 100 105 110
90 Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr Ala Gly Tyr Glu Gln
91 115 120 125
93 Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr Leu Leu Cys Arg
94 130 135 140
96 Pro Val Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
97 145 150 155 160
99 Leu Arg Ser Phe Ser Val Leu Ser Leu Ala Trp Gly Phe Ile Ala Asp
100 165 170 175
102 Val Asp Leu Glu Ser Asp Lys Tyr Arg Arg Leu Gly Glu Met Arg Phe
103 180 185 190
105 Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu Arg Thr Tyr Arg Gly
106 195 200 205
108 Arg Leu Ala Thr Leu Pro Val Gly Arg Val Gly Phe Lys Thr Pro Ala
109 210 215 220
111 Ser Pro Val Val Val Gln Gln Gly Pro Val Asp Ala His Leu Val Pro
112 225 230 235 240
114 Leu Glu Glu Gln Val Pro Ser His Trp Gln Val Val Pro Asp Glu Asp
115 245 250 255
117 Phe Val Leu Val Leu Ala Leu Leu His Ser His Leu Ala Ser Glu Met
118 260 265 270
120 Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly Val Met His Leu Phe
121 275 280 285
123 Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu Leu Arg Leu Phe Leu
124 290 295 300
126 Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu Cys Pro Tyr Leu Val

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132 Val Phe Ala Val Asp Gly Glu Leu Met Val Ser Glu Ala Val Gln Gly
133          340          345          350
135 Gln Val His Pro Asn Tyr Phe Trp Met Val Ser Gly Cys Val Glu Pro
136          355          360          365
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151 tgcgaagata gagatctggc cgccccgggg aatgacgagg gcgctcacac agcccaggga 180
152 ggtggagagg gcgagccac ggccagtcgc cagacaccct cctgggcaac accgataaga 240
153 agctgaacgc aggagccgcc gttacctcta gcagcgcggg ggcagcaccg gtggccctct 300
154 gtcagcggga gccccgggac ctggctatgg aaccagtaga atgccctcga ggactgctcc 360
155 cacggccatg cagagtgtct gtgctgtctga acccccaggg tggcaagggc aaggctctgc 420
156 agctcttcca gagccgtgtg cagcccttcc tggaggaggc agagataaacc tttaaactga 480
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183 <212> TYPE: PRT
184 <213> ORGANISM: Mus musculus
186 <400> SEQUENCE: 4

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187 Met Glu Pro Val Glu Cys Pro Arg Gly Leu Leu Pro Arg Pro Cys Arg
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190 Val Leu Val Leu Leu Asn Pro Gln Gly Gly Lys Gly Lys Ala Leu Gln
191           20           25           30
193 Leu Phe Gln Ser Arg Val Gln Pro Phe Leu Glu Glu Ala Glu Ile Thr
194           35           40           45
196 Phe Lys Leu Ile Leu Thr Glu Arg Lys Asn His Ala Arg Glu Leu Val
197           50           55           60
199 Cys Ala Glu Glu Leu Gly His Trp Asp Ala Leu Ala Val Met Ser Gly
200  65           70           75           80
202 Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
203           85           90           95
205 Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Gly Gly Ser
206           100          105          110
208 Gly Asn Ala Leu Ala Ala Ser Val Asn His Tyr Ala Gly Tyr Glu Gln
209           115          120          125
211 Val Thr Asn Glu Asp Leu Leu Ile Asn Cys Thr Leu Leu Leu Cys Arg
212          130          135          140
214 Arg Arg Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
215 145          150          155          160
217 Leu Arg Leu Tyr Ser Val Leu Ser Leu Ser Trp Gly Phe Val Ala Asp
218           165          170          175
220 Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu Gly Glu Ile Arg Phe
221           180          185          190
223 Thr Val Gly Thr Phe Phe Arg Leu Ala Ser Leu Arg Ile Tyr Gln Gly
224           195          200          205
226 Gln Leu Ala Tyr Leu Pro Val Gly Thr Val Ala Ser Lys Arg Pro Ala
227          210          215          220
229 Ser Thr Leu Val Gln Lys Gly Pro Val Asp Thr His Leu Val Pro Leu
230 225          230          235          240
232 Glu Glu Pro Val Pro Ser His Trp Thr Val Val Pro Glu Gln Asp Phe
233           245          250          255
235 Val Leu Val Leu Val Leu Leu His Thr His Leu Ser Ser Glu Leu Phe
236           260          265          270
238 Ala Ala Pro Met Gly Arg Cys Glu Ala Gly Val Met His Leu Phe Tyr
239           275          280          285
241 Val Arg Ala Gly Val Ser Arg Ala Ala Leu Leu Arg Leu Phe Leu Ala
242          290          295          300
244 Met Gln Lys Gly Lys His Met Glu Leu Asp Cys Pro Tyr Leu Val His
245 305          310          315          320
247 Val Pro Val Val Ala Phe Arg Leu Glu Pro Arg Ser Gln Arg Gly Val
248           325          330          335
250 Phe Ser Val Asp Gly Glu Leu Met Val Cys Glu Ala Val Gln Gly Gln
251           340          345          350
253 Val His Pro Asn Tyr Leu Trp Met Val Cys Gly Ser Arg Asp Ala Pro
254           355          360          365
256 Ser Gly Arg Asp Ser Arg Arg Gly Pro Pro Pro Glu Glu Pro
257          370          375          380
260 <210> SEQ ID NO: 5

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261 <211> LENGTH: 1840

262 <212> TYPE: DNA

263 <213> ORGANISM: Homo sapiens

265 <400> SEQUENCE: 5

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268 tacgctttta cagttcactg tgtaaagaga gcacgacggc accgctggaa gtggcgcgag 180
269 gtgactttct ggtgtccaga ggagcagctg tgtcacttgt ggctgcagac cctgcgggag 240
270 atgctggaga agctgacgtc cagaccaaag catttactgg tatttatcaa cccgtttgga 300
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273 gaacatgcta atcaggccaa ggagactctg tatgagatta acatagacaa atacgacggc 480
274 atcgtctgtg tcggcgagga tggatgttc agcgaggtgc tgcacggctc gattgggagg 540
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276 ctccggattg gaatcattcc cgagggtca acggactgcg tgtgttactc caccgtgggc 660
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301 <212> TYPE: PRT

302 <213> ORGANISM: Homo sapiens

304 <400> SEQUENCE: 6

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311 Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu Met Leu Glu Lys
312 35 40 45
314 Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly
315 50 55 60
317 Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu

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